

SARS-CoV-2 Sequencing and Variants in Washington State

Washington State Department of Health

May 18, 2022



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Next generation sequencing is a set of laboratory methods that scientists use to scan a viral genome to determine the genome sequence of a virus. A genome sequence of a virus is referred to as its “genomic fingerprint,” and can reveal mutations in a virus that make it unique. Mutations are changes in a genome sequence and occur naturally over time.

Scientists compare viral genomes to better understand how viruses can spread from person to person. Sequencing allows public health officials to detect clusters of cases, and monitor new lineages. Groups of same-species viruses that share a set of genome mutations are referred to as a lineage. Some lineages may have characteristics such as the ability to spread more quickly, or cause more severe disease. These lineages are classified as variants of interest, variants being monitored, or variants of high concern.

Throughout this report, we refer to the scientific name of the virus SARS-CoV-2 that causes COVID-19. Sequencing can only be performed on samples that are processed in laboratories and where swabs are stored in liquid that is compatible with sequencing, which means only samples used for molecular tests (such as PCR) can be included. For this reason, this report is limited to confirmed cases only. The genomes that are sequenced and compared are those of the virus, not humans.

At a glance (data through May 17, 2022)

- During the month of April 2022, **13.8%** of all confirmed molecular COVID-19 cases were sequenced. This number is preliminary and will change over time as additional specimens are received from the previous month.
- **92,893 (8.7%)** COVID-19 cases in Washington state have sequencing information available since January 2021.

CDC currently categorizes variants as Variants of High Consequence (VOHC), Variants of Concern (VOC), Variants of Interest (VOI) and Variants Being Monitored (VBM). There are currently no VOHC and VOI so only VOC and VBM are detailed in this report.

Variants of Concern

Variant	Area first detected	Background	Cumulative Washington cases detected	First detection in Washington*	Most recent detection in Washington*
Omicron (B.1.1.529 and BA lineages)	South Africa	Early research indicates evidence for increased transmissibility, immune evasion, and lower risk of hospitalization and death, relative to Delta. Approved vaccines are effective at preventing severe disease and death, including against the Omicron variant.	22,085	Nov 29, 21	May 02, 22

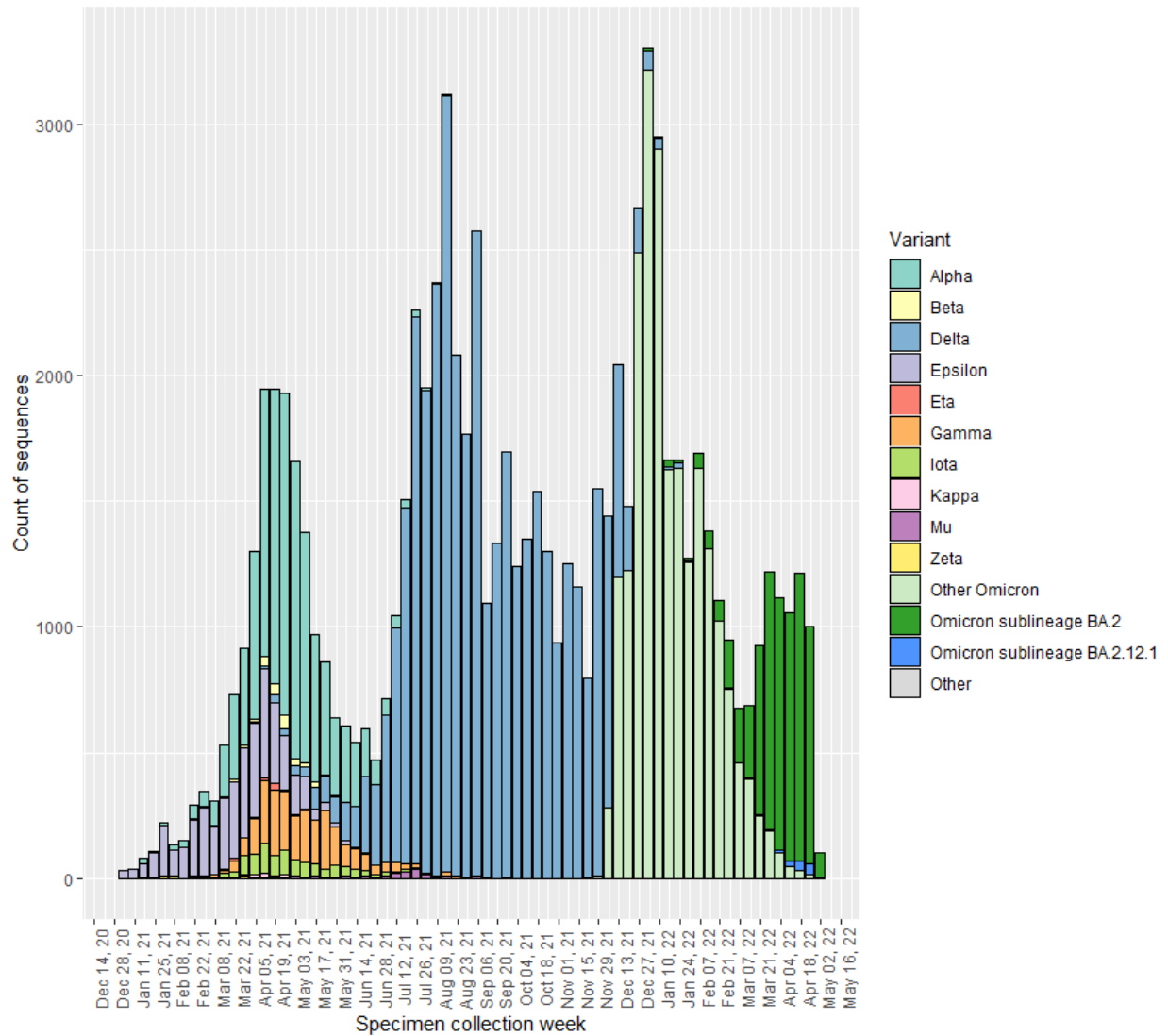
*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

Variants Being Monitored

Variant	Area first detected	Cumulative Washington cases detected	First detection in Washington*	Most recent detection in Washington*
Alpha (B.1.1.7)	United Kingdom	9,937	Jan 07, 21	Sep 08, 21
Beta (B.1.351)	South Africa	272	Jan 29, 21	Jun 29, 21
Delta (B.1.617.2 and AY lineages)	India	38,171	Apr 03, 21	Feb 28, 22
Epsilon (B.1.427 / B.1.429)	California	4,047	Dec 11, 20	Jun 24, 21
Eta (B.1.525)	New York	83	Feb 02, 21	Jun 08, 21
Gamma (P.1)	Brazil	2,401	Feb 06, 21	Dec 02, 21
Iota (B.1.526)	New York	896	Jan 21, 21	Aug 20, 21
Kappa (B.1.617.1)	India	46	Mar 22, 21	Jun 14, 21
Mu (B.1.621)	Colombia	184	Apr 09, 21	Dec 20, 21
Zeta (P.2)	Brazil	44	Jan 18, 21	Apr 20, 21

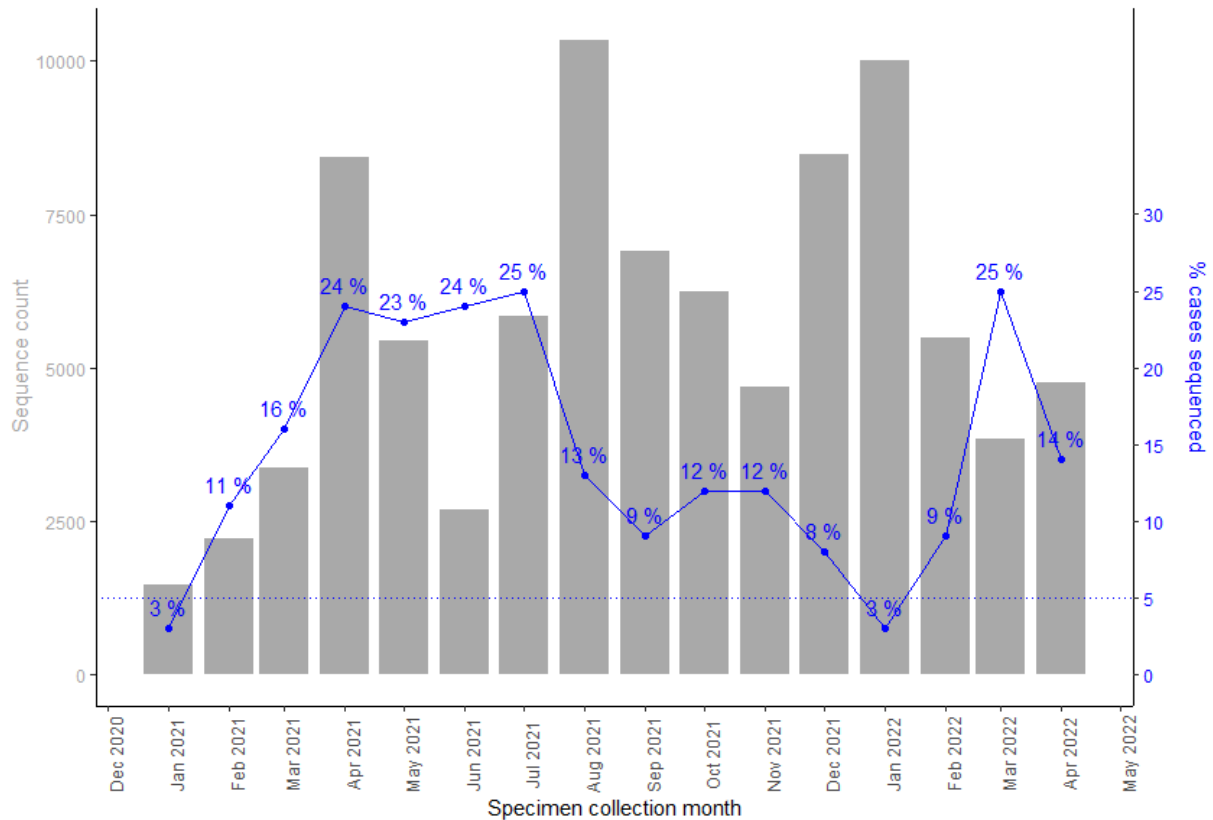
*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

Epidemiologic curve of variants being monitored and variants of concern by week of specimen collection date from January 01, 2021 to May 07, 2022



- The above graph shows the total number of variants detected by the week the specimen was collected from a patient.
- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced.
- This graph shows all specimens sequenced, including specimens sequenced during outbreaks and other targeted sequencing efforts.

Number of specimens sequenced, and percent of Washington State confirmed COVID-19 cases that have been sequenced by specimen collection date from January 2021 through April 2022.

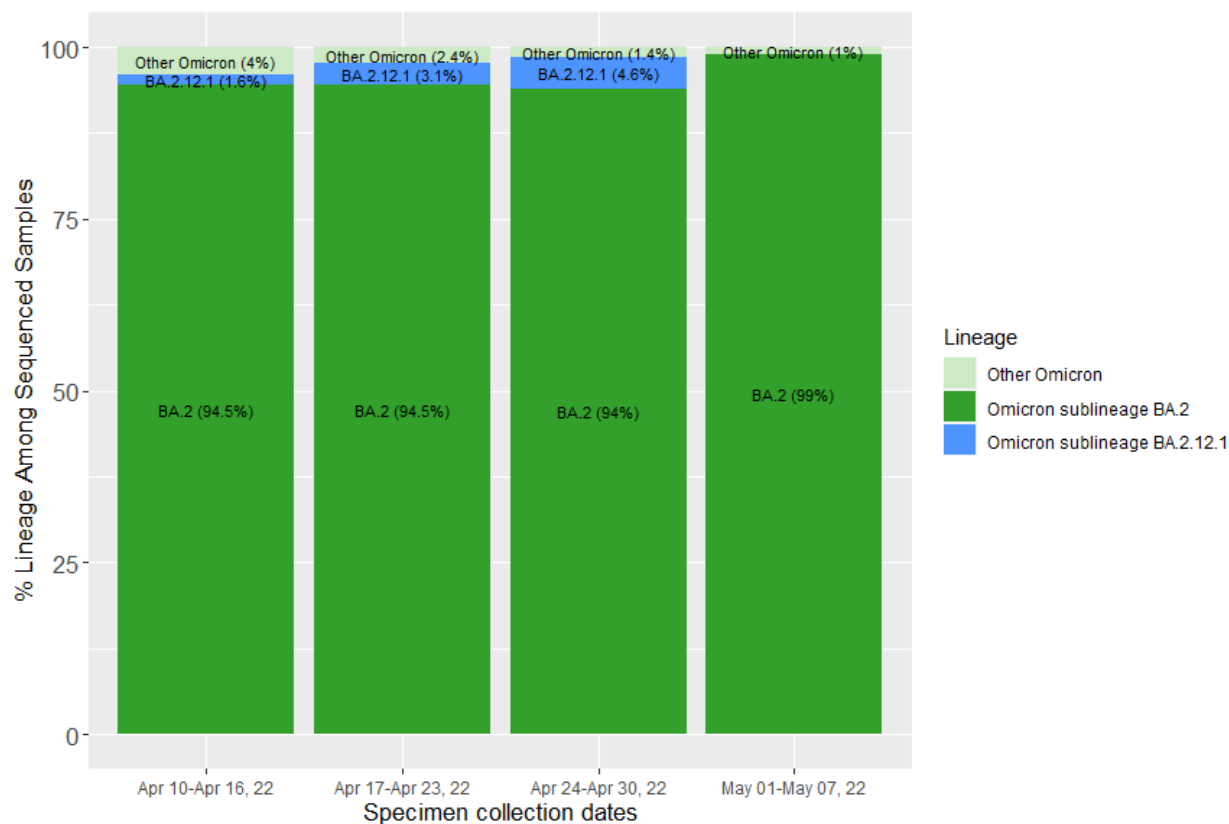


- Samples are not sequenced for every confirmed COVID-19 case. The above graph shows the total number of specimens sequenced (gray bars) and the percent of all confirmed cases (blue line) that have had sequencing performed each month. Data from the previous month may still be incomplete.
- Sequencing can be performed on stored specimens at any time, so numbers from past months may change if stored specimens are sequenced.

SARS-CoV-2 Lineages Circulating in Washington State

The graph below shows the change in proportion of select SARS-CoV-2 lineages by time period. A viral lineage is a group of viruses that descend from a common ancestor with shared genetic characteristics, allowing them to be grouped together. As the proportions of variants increase, the proportion of other lineages will decrease.

NOTE: The data on this graph come from cases that are randomly selected for sequencing statewide. Cases sequenced because they were part of an outbreak or were otherwise manually selected for sequencing are excluded.



The chart above shows the proportions of the most common SARS-CoV-2 lineages circulating in Washington grouped in one-week intervals. Proportions are calculated using data which are subject to change over time and will be updated as more data becomes available, including data from prior time periods. **Due to the time it takes to complete sequencing, the most recent time period is based on a very small number of sequences and likely to be adjusted over time.**

To see the national trends, visit the CDC's [variant proportions page](#).

The table below shows the current variants of concern (VOC) that have been detected by county of home address since January 2022.

County	VOC			Total VOC specimens sequenced
	Other Omicron	BA.2	BA.2.12.1	
Adams	1	0	0	65
Asotin	0	0	0	13
Benton	11	32	0	589
Chelan	3	14	0	186
Clallam	0	106	2	309
Clark	1	133	0	478
Columbia	0	1	0	7
Cowlitz	8	21	0	339
Douglas	1	8	0	120
Ferry	0	1	0	10
Franklin	6	8	0	397
Grant	2	2	0	266
Grays Harbor	15	46	0	457
Island	0	58	2	128
Jefferson	0	14	0	81
King	35	4,119	68	10,502
Kitsap	2	107	0	376
Kittitas	0	6	0	73
Klickitat	0	2	0	20
Lewis	13	9	0	250
Lincoln	0	1	0	7
Mason	1	16	0	110
Okanogan	1	1	0	125
Pacific	6	2	0	119
Pend Oreille	0	0	0	13
Pierce	11	359	0	1,586

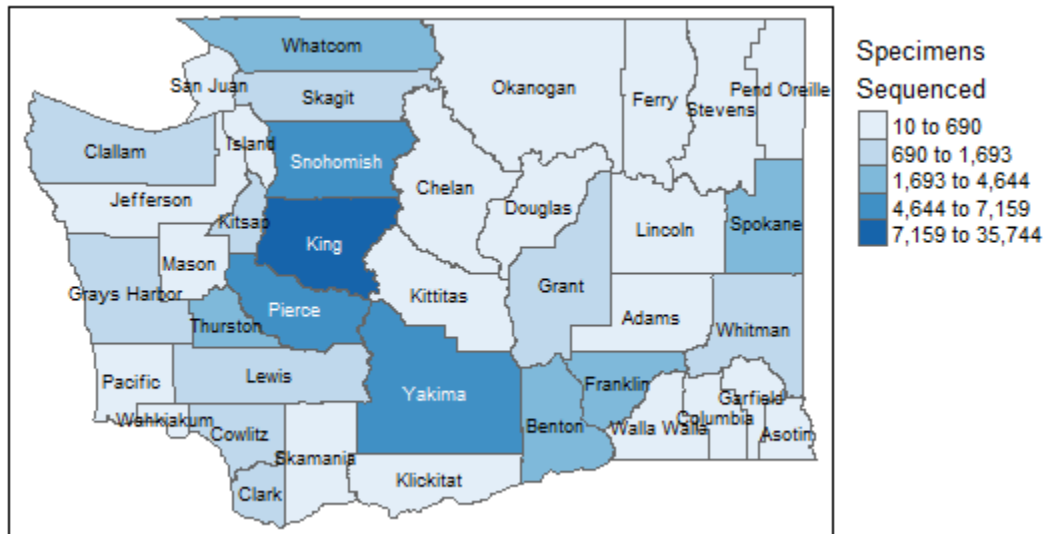
County	VOC			Total VOC specimens sequenced
	Other Omicron	BA.2	BA.2.12.1	
San Juan	0	2	0	18
Skagit	0	131	8	303
Skamania	0	1	0	6
Snohomish	4	707	12	1,793
Spokane	15	60	0	768
Stevens	1	1	0	29
Thurston	14	105	1	1,351
Wahkiakum	0	3	0	10
Walla Walla	1	13	0	177
Whatcom	2	742	29	1,401
Whitman	1	7	0	192
Yakima	11	31	2	1,356

In this table, "Other Omicron" includes all B.1.1.529 and BA.1, BA.3, BA.4 and BA.5 sublineages

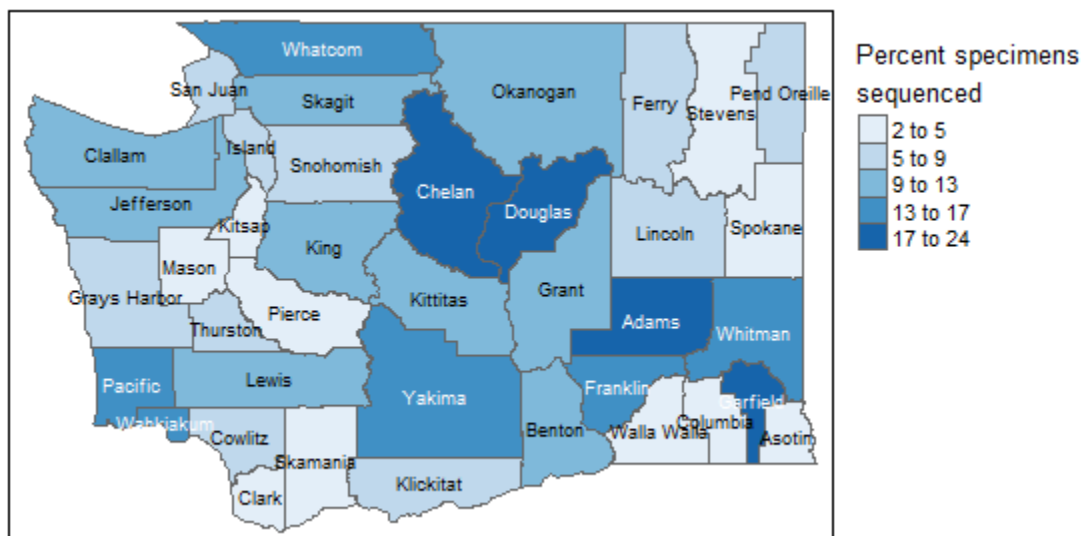
Geographic Coverage of Sequencing

Efforts are made to sequence specimens from all geographic areas of Washington State. The number of sequences and the percent of cases sequenced vary based on several factors including which laboratories conduct the majority of testing in each locality.

The map below shows the number of specimens sequenced by county of home address since January 1, 2021.



The map below shows the percent of COVID-19 cases with at least one specimen sequenced by county of home address since January 1, 2021.



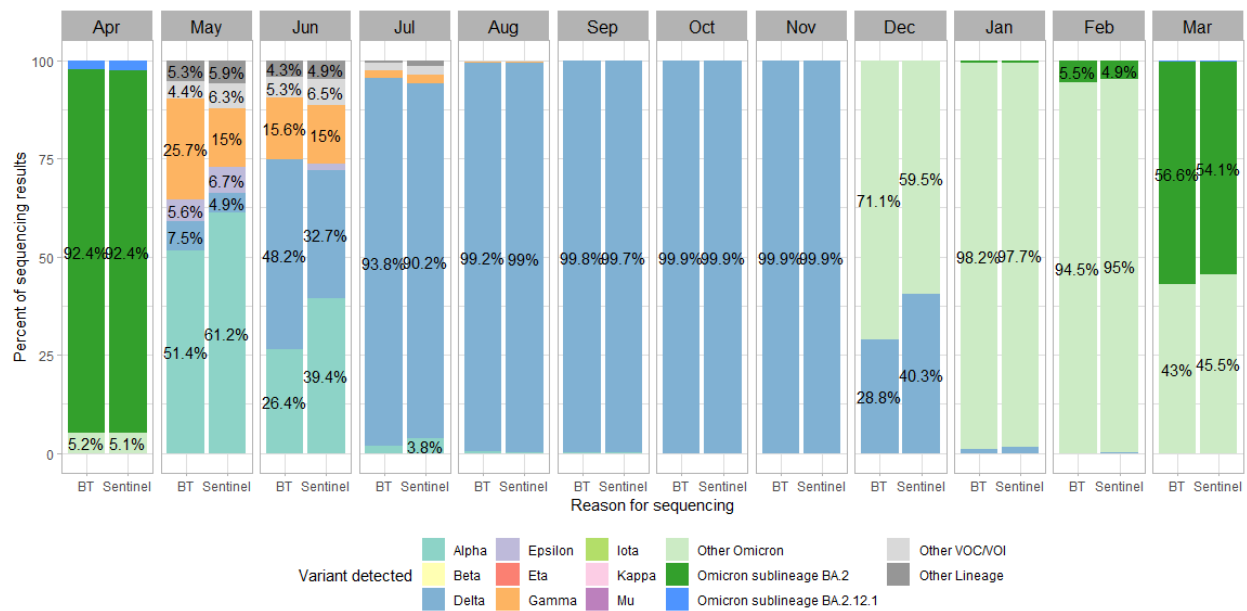
Vaccine Breakthrough Cases

A complete report on vaccine breakthrough cases can be found in the reports section of the [DOH data dashboard](#).

A vaccine breakthrough case is defined as someone who tests positive for SARS-CoV-2 at least 14 days after their final dose of SARS-CoV-2 vaccine. DOH is monitoring sequencing results for vaccine breakthrough cases. This can help scientists determine whether any specific variants of the virus are causing more breakthrough cases than expected.

The table and chart below show vaccine breakthrough cases based on lineages. Lineages not designated as VOC, VOI or VBM are marked as 'other'.

Proportion of variants identified among vaccine breakthrough cases (Breakthrough) with sequencing results compared to variants identified among randomly selected COVID-19 cases (Sentinel) during the same time frame



Breakthrough cases by variant table

Variant	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Jan	Feb	Mar
Alpha	138	164	105	30	9	1	0	0	0	0	0	0
Delta	3	24	192	1,658	2,937	2,015	2,178	1,654	1,294	56	0	0
Epsilon	82	18	1	0	0	0	0	0	0	0	0	0
Gamma	53	82	62	33	6	0	0	0	1	0	0	0
Other Omicron	176	0	0	0	0	0	0	1	3,189	5,267	2,959	1,172
Omicron sublineage BA.2	3,150	69	0	0	0	0	0	0	0	39	172	1,544
Omicron sublineage BA.2.12.1	83	0	0	0	0	0	0	0	0	0	0	6

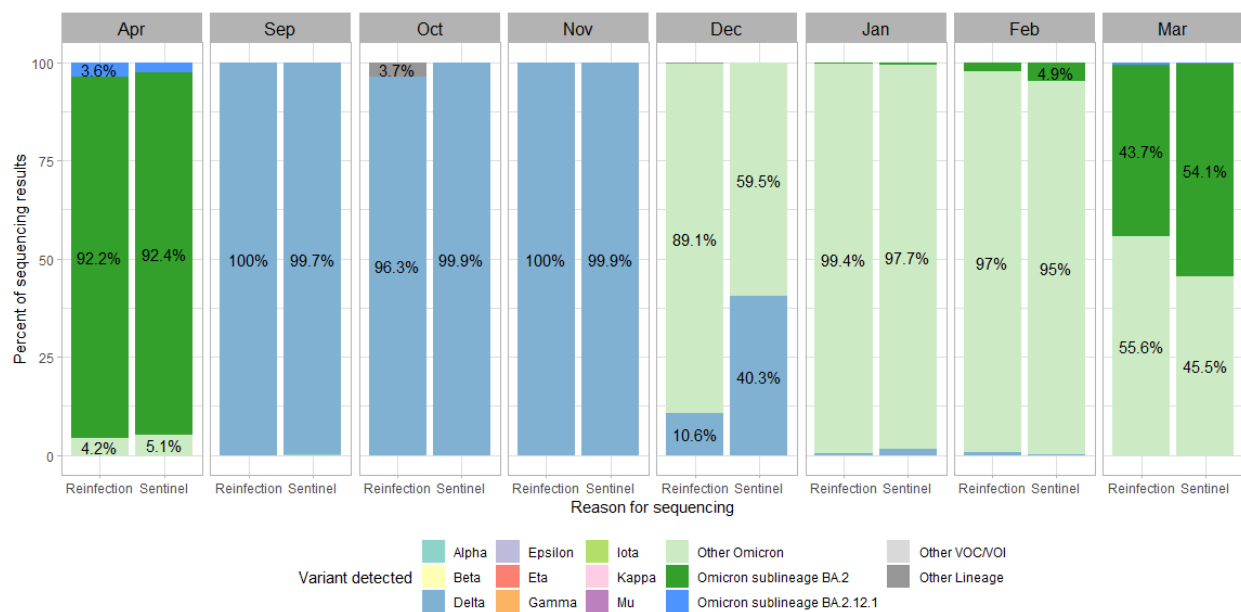
Variant	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Jan	Feb	Mar
Other VOC/VOI	22	14	21	34	6	3	0	0	0	0	0	0
Other Lineage	28	17	17	13	4	0	2	1	3	4	1	5

Reinfection

A complete report on reinfection cases can be found in the reports section of the DOH data dashboard.

In general, reinfection means a person was infected once with the virus that causes COVID-19, recovered, and then later became infected again. We are still learning about COVID-19 and the duration and strength of immunity following infection with this virus. Based on what we know from similar respiratory viruses, we expect some COVID-19 reinfections to occur. For disease surveillance purposes, a person with a reported reinfection is an individual with two positive COVID-19 test results (molecular or antigen) reported to DOH where the tests were performed at least 90 days apart. In addition, if genetic sequencing of respiratory samples from a patient's first (or primary) infection and most recent infection identifies different variants, they are considered a confirmed reinfection regardless of the amount of time between positive tests. Washington State Department of Health adopted this definition on September 1, 2021.

DOH is monitoring sequencing results for reinfection cases. This can help scientists determine whether any specific variants of the virus are causing more reinfection cases than expected. The table and chart below show reinfection cases based on lineages. Lineages not designated as VOC, VOI or VBM are marked as 'other'. Proportion of variants identified among reinfection cases (Reinfection) with sequencing results compared to variants identified among randomly selected COVID-19 cases (Sentinel) during the same time frame.



Reinfection cases by variant table

Please note - data for the most recent month are incomplete

Variant	Apr	May	Sep	Oct	Nov	Dec	Jan	Feb	Mar
Delta	0	0	32	52	46	28	2	2	0
Other Omicron	7	0	0	0	0	236	620	290	79
Omicron sublineage BA.2	153	5	0	0	0	0	1	7	62

Variant	Apr	May	Sep	Oct	Nov	Dec	Jan	Feb	Mar
Omicron sublineage BA.2.12.1	6	0	0	0	0	0	0	0	1
Other Lineage	0	0	0	2	0	1	1	0	0

The hospitalization table below includes data since January 1, 2021 and does not account for factors that can influence hospitalization rates such as age and vaccination status, which may be different across variants. This means that hospitalization rates are not necessarily comparable between variants.

Hospitalizations and deaths by variant

Variant	Cases who were hospitalized	Cases who died from COVID-19	Total cases
Other Omicron	1.3%	0.5%	22,054
BA.2	0.5%	0.1%	6,870
BA.2.12.1	0%	0%	124
Alpha	3.4%	0.5%	9,910
Beta	6.3%	0.4%	271
Delta	4.2%	1.3%	38,074
Epsilon	2.6%	0.7%	3,996
Gamma	6.7%	1.6%	2,386
Iota	3.1%	1.1%	893
Mu	3.3%	2.2%	183
Other	2.5%	0.7%	4,814

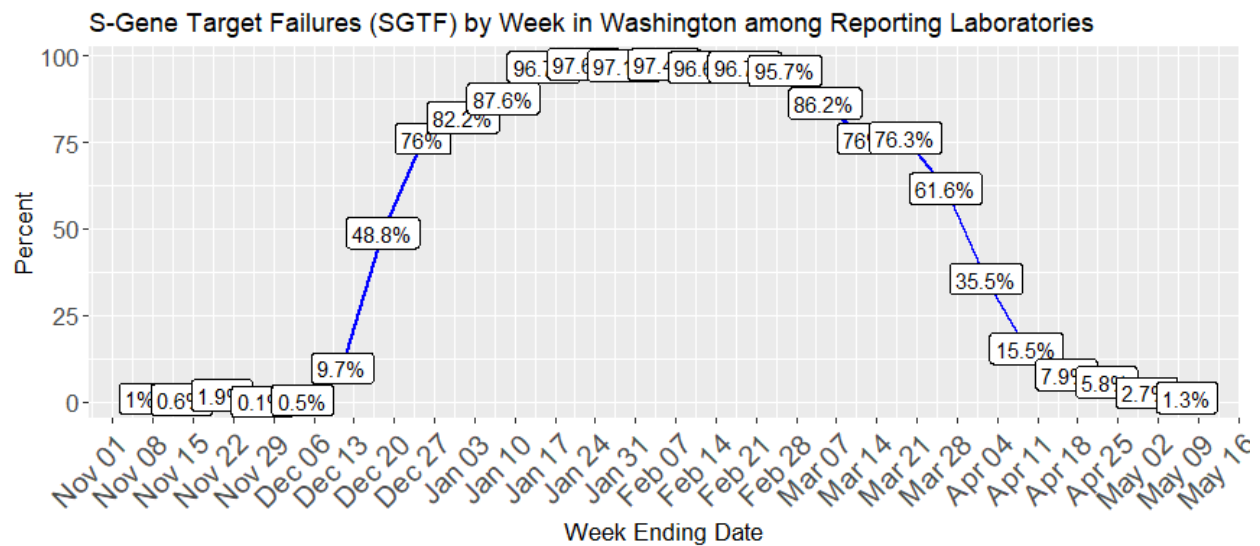
Age distribution by variant

Variant	Age 0-19	Age 20-34	Age 35-49	Age 50-64	Age 65-79	Age 80+	Unknown	Total cases
Other Omicron	24%	32%	22%	13%	5%	2%	2%	22,054
BA.2	19%	34%	23%	14%	7%	2%	2%	6,870
BA.2.12.1	28%	23%	17%	14%	10%	3%	5%	124
Alpha	27%	32%	22%	12%	3%	1%	2%	9,910
Beta	30%	35%	21%	11%	3%	0%	1%	271
Delta	23%	29%	22%	14%	7%	2%	2%	38,074
Epsilon	25%	31%	22%	14%	4%	1%	2%	3,996
Gamma	22%	35%	23%	11%	4%	3%	2%	2,386
Iota	25%	32%	24%	12%	4%	1%	1%	893
Mu	23%	37%	19%	12%	7%	1%	2%	183
Other	24%	29%	23%	15%	5%	2%	2%	4,814

*Other includes all viruses that are not categorized as VOC or VBM

Tracking Omicron Using Clinical Tests

WA DOH is tracking the Omicron variant using sequencing. One challenge is that the sequencing process can take up to a few weeks, so we use another testing marker known as 'S gene target failure (SGTF)' to identify possible Omicron cases carrying this mutation rapidly and inform public health action. BA.2 and BA.2.12.1 do not carry this mutation. While SGTF does not always mean that a case will be finalized as Omicron, greater than 95% of these results are predicted to finalize as Omicron. Many laboratories are sharing this data with WA DOH to help track the spread of Omicron.



A small number of other SARS-CoV-2 viruses other than Omicron can cause SGTF, these can be seen in the small numbers (0-3) seen weekly prior to the week of November 28th. Additionally, the Omicron sub-lineage BA.2 and BA.2.12.1 do not carry this mutation.

First Day of Week	Last Day of Week	Total Positives	Total SGTF	Percent SGTF
2021-10-31	2021-11-06	1,249	13	1%
2021-11-07	2021-11-13	1,231	8	0.6%
2021-11-14	2021-11-20	1,240	24	1.9%
2021-11-21	2021-11-27	1,363	2	0.1%
2021-11-28	2021-12-04	2,578	13	0.5%
2021-12-05	2021-12-11	2,483	242	9.7%
2021-12-12	2021-12-18	3,304	1,614	48.8%
2021-12-19	2021-12-25	5,200	3,951	76%
2021-12-26	2022-01-01	6,484	5,329	82.2%
2022-01-02	2022-01-08	15,588	13,657	87.6%
2022-01-09	2022-01-15	16,599	16,050	96.7%

First Day of Week	Last Day of Week	Total Positives	Total SGTF	Percent SGTF
2022-01-16	2022-01-22	13,375	13,058	97.6%
2022-01-23	2022-01-29	8,895	8,640	97.1%
2022-01-30	2022-02-05	4,893	4,767	97.4%
2022-02-06	2022-02-12	2,794	2,700	96.6%
2022-02-13	2022-02-19	1,433	1,385	96.7%
2022-02-20	2022-02-26	674	645	95.7%
2022-02-27	2022-03-05	508	438	86.2%
2022-03-06	2022-03-12	367	279	76%
2022-03-13	2022-03-19	337	257	76.3%
2022-03-20	2022-03-26	375	231	61.6%
2022-03-27	2022-04-02	332	118	35.5%
2022-04-03	2022-04-09	381	59	15.5%
2022-04-10	2022-04-16	544	43	7.9%
2022-04-17	2022-04-23	762	44	5.8%
2022-04-24	2022-04-30	1,143	31	2.7%
2022-05-01	2022-05-07	1,190	15	1.3%

We thank the reporting laboratories: University of Washington Virology, Northwest Laboratories, The Vancouver Clinic, Atlas Laboratories, Evergreen Health, FidaLab

We gratefully acknowledge the GISAID initiative, original laboratories responsible for obtaining the specimens, as well as the submitting laboratories where the genome data were generated and shared via GISAID.

The following clinical laboratories have contributed specimens for sequencing:

Aegis Sciences Corporation
Allenmore Hospital Laboratory
Altius Institute for Biomedical Sciences
Atlas Genomics
BioReference Laboratories Inc.
Cascade Valley Hospital
Central Washington Hospital
Columbia Basin Hospital
Curative Labs Inc.
Dayton General Hospital
Deaconess Hospital
Diatherix Laboratories
Dynacare Northwest Inc.
East Adams Rural Hospital
Everett Clinic Microbiology
Evergreen Healthcare
Ferry County Hospital
FidaLab
Forks Community Hospital
Fulgent Genetics
Gravity Diagnostics, LLC
Harborview Medical Center
Healthquest Esoterics
Helix/Illumina
Incyte Diagnostics Spokane

Infinity Biologix
Interpath Laboratory
Jefferson Healthcare
Kaiser Permanente Washington Health Research Institute
Labcorp
Laboratories Northwest
Laboratory Corporation of America
Legacy Laboratory
Magnolia Diagnostics, LLC
Mann-Grandstaff VA Medical Center
Mason General Hospital Laboratory
Mid Valley Hospital
Molecular Testing Labs
MultiCare
Northwest Laboratories
Northwest Laboratories
OHSU Lab Services Molecular Microbiology Lab
Olympic Medical Center
Overlake Hospital
PeaceHealth
Polyclinic
Premier Medical Laboratory
Providence Medical Group
Public Health Seattle-King County Laboratory
Quest Diagnostics Incorporated
Samaritan Hospital Lab
Seattle & King County Public Health Lab
Seattle Children's Hospital

Seattle Flu Study
Skagit Valley Hospital Laboratory
St. Francis Hospital
St. Joseph Medical Center Microbiology
St. Michael Medical Center Laboratory
Swedish Medical Center
Tacoma General Hospital
The Vancouver Clinic
Tomorrow's Health, LLC
TridentCare Laboratory
TridentCare Laboratory
University of Washington Virology Lab
Virginia Mason Franciscan Health Microbiology
Washington State Department of Health Public Health Laboratories

The following labs have reported sequencing data that is included in this report:

Aegis Laboratory
Altius Institute for Biomedical Research
Atlas Genomics
Boise VA Medical Center
Centers for Disease Control and Prevention
Curative
Flow Diagnostics
Fulgent Genetics
Ginkgo Bioworks Clinical Laboratory
Gravity Diagnostics, LLC
Gritman Medical Center
Grubaugh Lab
Helix Laboratories

Idaho Bureau of Laboratories
Infinity Biologix
Institute for Systems Biology
Kaiser Permanente
Laboratory Corporation of America
Montana Public Health Laboratory
Naval Health Research Center
Oregon SARS-CoV-2 Genome Sequencing Center
Oregon State Public Health Laboratory
Providence St. Joseph Health Molecular Genomics Laboratory
Quest Diagnostics
Seattle Flu Study
The Jackson Laboratory
The Loring Laboratory
United States Army Medical Research Institute of Infectious Diseases
University of Washington Virology Lab
Washington State Department of Health Public Health Laboratories
